

SEQUENCE LISTING

<110> Bermudes, G.  
King, I.  
Clairmont, C.  
Lin, S.  
Belcourt, M.

<120> COMPOSITIONS AND METHODS FOR TUMOR-TARGETED  
DELIVERY OF EFFECTOR MOLECULES

<130> 8002-059

<150> 60/157,581  
<151> 1999-10-04

<150> 60/157,637  
<151> 1999-10-04

<160> 61

<170> FastSEQ for Windows Version 3.0

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<220>  
<223> Forward primer

<400> 1

gaagatcttc cggaggaggg gaaatg

26

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<220>  
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<400> 2

cgggatccga gctcgagggc ccgggaaagg atctaagaag atcc

44

<210> 3  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1) ... (474)

<400> 3

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1 5 10 15	
gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	96
20 25 30	
cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	144
35 40 45	
ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg Leu Val Val Pro Ser Glu Gly Leu Tyr Ile Tyr Ser Gln Val Leu	192
50 55 60	
ttc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	240
65 70 75 80	
atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	288
85 90 95	
gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	336
100 105 110	
aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Val Phe Gln Leu Glu	384
115 120 125	
aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	432
130 135 140	
ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu	474
145 150 155	
taa	477
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<213> Homo sapiens	
<400> 4	
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Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Ile Tyr Ser Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	

Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser  
85 90 95  
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala  
100 105 110  
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu  
115 120 125  
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp  
130 135 140  
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
145 150 155

<210> 5  
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<220>  
<223> Forward primer

<400> 5  
ccgacgcgtt gacacctgaa aactggag

28

<210> 6  
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<220>  
<223> Reverse primer

<400> 6  
ccgacgcgtg aaaggatctc aagaagatc

29

<210> 7  
<211> 543  
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<220>  
<223> Fusion construct

<221> CDS  
<222> (1)...(540)

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Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
1 5 10 15

48

acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc  
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser  
20 25 30

96

gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag  
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln  
35 40 45

144

ctg cag tgg ctg aac cgt cgc gct aac gcc ctg gca aac ggc gtt	192
Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val	
50 55 60	
gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg	240
Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu	
65 70 75 80	
atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat	288
Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His	
85 90 95	
gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc	336
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr	
100 105 110	
aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act	384
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr	
115 120 125	
ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt	432
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly	
130 135 140	
ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac	480
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn	
145 150 155 160	
cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt	528
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly	
165 170 175	
att atc gca ctg taa	543
Ile Ile Ala Leu	
180	

<210> 8  
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 <213> Artificial Sequence .

<400> 8  
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 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser  
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 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln  
 35 40 45  
 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val  
 50 55 60  
 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu  
 65 70 75 80  
 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His  
 85 90 95  
 Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr  
 100 105 110

Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr  
 115 120 125  
 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly  
 130 135 140  
 Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn  
 145 150 155 160  
 Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly  
 165 170 175  
 Ile Ile Ala Leu  
 180

<210> 9  
 <211> 801  
 <212> DNA  
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<220>  
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<221> CDS  
 <222> (1)...(798)

<400> 9  
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 Met Lys Lys Thr Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
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 acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac 96  
 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp  
 20 25 30  
 aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt 144  
 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser  
 35 40 45  
 tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa 192  
 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln  
 50 55 60  
 gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc 240  
 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr  
 65 70 75 80  
 tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct 288  
 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser  
 85 90 95  
 ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act 336  
 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr  
 100 105 110  
 ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat 384  
 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn  
 115 120 125  
 gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt 432  
 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser  
 130 135 140

ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc	480	
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val		
145 150 155 160		
atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga	528	
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg		
165 170 175		
ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc	576	
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val		
180 185 190		
caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg	624	
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met		
195 200 205		
aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc	672	
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu		
210 215 220		
tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga	720	
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg		
225 230 235 240		
att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa	768	
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu		
245 250 255		
gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa	801	
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly		
260 265		
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1 5 10 15		
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp		
20 25 30		
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser		
35 40 45		
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln		
50 55 60		
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr		
65 70 75 80		
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser		
85 90 95		
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr		
100 105 110		
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn		
115 120 125		
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser		
130 135 140		

Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val  
 145 150 155 160  
 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg  
 165 170 175  
 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val  
 180 185 190  
 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met  
 195 200 205  
 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu  
 210 215 220  
 Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg  
 225 230 235 240  
 Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu  
 245 250 255  
 Ala Ser Phe Phe Gly Ala Phe Leu Val Gly  
 260 265

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<211>-465

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion construct

<221> CDS

<222> (1)...(462)

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Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Ala Leu Thr	
1 5 10 15	

agt gta gcg cag gcc gct cct act agc tcg agc act aag aaa act caa	96
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln	
20 25 30	

ctg caa ttg gag cat ctg ctg gat ctg cag atg att ctg aat ggc	144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly	
35 40 45	

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa	192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys	
50 55 60	

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg	240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu	
65 70 75 80	

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct	288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser	
85 90 95	

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta	336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val	
100 105 110	

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384  
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
115 120 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432  
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
130 135 140

ttt gcc caa tcg atc att agc acg tta act taa 465  
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
145 150

<210> 12  
<211> 154  
<212> PRT  
<213> Artificial Sequence

<400> 12

Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Ala Leu Thr  
1 5 10 15  
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln  
20 25 30  
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly  
35 40 45  
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys  
50 55 60  
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu  
65 70 75 80  
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser  
85 90 95  
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val  
100 105 110  
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
115 120 125  
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
130 135 140  
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
145 150

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<212> DNA  
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<221> CDS  
<222> (1)...(462).

<400> 13

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1 5 10 15

agt gtg gcc aaa gct cct act agc tcg agc act aag aaa act caa Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln	96
20 25 30	
ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly	144
35 40 45	
atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys	192
50 55 60	
ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu	240
65 70 75 80	
gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser	288
85 90 95	
aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val	336
100 105 110	
atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr	384
115 120 125	
gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr	432
130 135 140	
ttt gcc caa tcg atc att agc acg tta act taa Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr	465
145 150	
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<212> PRT	
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Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr	
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20 25 30	
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly	
35 40 45	
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys	
50 55 60	
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu	
65 70 75 80	
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser	
85 90 95	
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val	
100 105 110	

Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr  
115 120 125  
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr  
130 135 140  
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr  
145 150

<210> 15  
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<212> DNA  
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<223> Forward primer

<400> 15

agtctagaca atcaggcgaa gaacgg

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<210> 16  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse primer

<400> 16

agccatggag tcaccctcac tttc

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<210> 17  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Forward primer

<400> 17

ggatccttaa gaccacttt cacatttaag t

31

<210> 18  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse primer

<400> 18

ggttccatgg ttcaacttttc tctatcac

28

<210> 19  
<211> 33  
<212> DNA  
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<220>  
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 <212> DNA  
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 <213> Artificial Sequence  
 <220>  
 <223> Forward primer  
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 gtgtccatgg ctcggcgccc aagtgtcgaa actgaccatc atcatcatca tcatacacagg 60  
 caccgcact tc 72  
 <210> 22  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Reverse primer  
 <400> 22  
 gtgcggatcc ctacttggag gcagtcatga agctg 35  
 <210> 23  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens  
 <400> 23  
 Met Ala Arg Arg Ala Ser Val Gly Thr Asp His His His His His His  
 1. . . . . 5 . . . . . 10 . . . . . 15  
 <210> 24  
 <211> 22  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Peptide sequence TiP 13.40  
 <400> 24

Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg  
1 5 10 15  
Val Val Met Tyr Glu Gly  
20

<210> 25  
<211> 66  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Nucleotide sequence encoding TiP13.40

<400> 25  
gcgtaccgct ggccctgtc ccatcgcccg aaaaccggct ttatccgcgt ggtgatgtac 60  
gaaggc 66

<210> 26  
<211> 101  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide

<400> 26  
gtgtactagt gtggcgcaagg cggcgttaccg ctggcgccctg tcccatcgcc cgaaaaccgg 60  
ctttatccgc gtggtgatgt acgaaggcta aggatccgcg c 101

<210> 27  
<211> 101  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide

<400> 27  
gcgcggatcc tttagccttcg tacatcacca cgcggataaa gccggtttc gggcgatggg 60  
acaggcgcca gcggtacgcc gcctgcgcca cactagtaca c 101

<210> 28  
<211> 101  
<212> PRT  
<213> Homo sapiens

<400> 28  
Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe  
1 5 10 15  
Leu Gly Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu  
20 25 30  
Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser  
35 40 45  
Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly  
50 55 60  
Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg  
65 70 75 80

Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys  
85 90 95  
Lys Leu Leu Glu Ser  
100

<210> 29  
<211> 106  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 29  
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gtacaaaaaa atcatcaaaa aactgctgga aagctaaggta tccgcg 106

<210> 30  
<211> 106  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 30  
cgcggatcc tagctttcca gcagttttt gatgatttt ttgtacagcg ggcgcctgcag 60  
gtccaggcag atttgcggc cgttcgcctg cgccacacta gtgaag 106

<210> 31  
<211> 85  
<212> PRT  
<213> Homo sapiens

<400> 31  
Ile Tyr Ser Phe Asp Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro  
1 5 10 15  
Gln Lys Val Ile Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val  
20 25 30  
Asp Asn Tyr Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly  
35 40 45  
Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr  
50 55 60  
Ser Cys Ala Asn Arg Leu Ile Val Leu Cys Ile Glu Asn Ser Phe Met  
65 70 75 80  
Thr Asp Ala Arg Lys  
85

<210> 32  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 32  
ggcttcacta gtgtggcgca ggcgatatac tcctttatgc gtcg 44

<210> 33  
<211> 37  
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<210> 47

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<212> DNA

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33

<210> 48

<211> 33

<212> DNA

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<223> Reverse primer

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<220>  
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 <223> n=a, c, g, or t

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130

<210> 59  
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<212> DNA  
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<223> n=a, c, g, or t  
  
<221> CDS  
<222> (7)...(427)

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48

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96

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144

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Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr  
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192

ctg tcc ctg tgc ggc tgc gcg aac gcg cgc gcg acc ctg cgc tcc  
Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser  
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240

gcg acc gcg gat aac tcc gaa aac acc ggc ttt aaa aac gtc ccg gat  
Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp  
80 85 90

288

ctg cgc acc gat cag ccg aaa ccg ccg tcc aaa aaa cgc tcc tgc gat  
Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp  
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336

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Pro Ser Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr  
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384

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427

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444

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<213> Bacteriophage

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Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser		
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Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr		
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Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg		
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